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Genome-wide association study identifies a putative variant in MYO3B and common variants in PTPRT associated with bovine tuberculosis

Citation for published version:

Bermingham, M, *Genome-wide association study identifies a putative variant in MYO3B and common variants in PTPRT associated with bovine tuberculosis: Front cover of Heredity February 2014, 2014, Digital or Visual Products.*

Link:

[Link to publication record in Edinburgh Research Explorer](#)

Document Version:

Early version, also known as pre-print

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Heredity

The official journal of the Genetics Society

Volume 112
Number 5
May 2014
www.nature.com/hdy



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nature publishing group 